

Supplementary material 3

Prediction of nuclear localization signals in putative Z-DNA/Z-RNA binding proteins, cNLS Mapper webserver was used (http://nls-mapper.iab.keio.ac.jp/cgi-bin/NLS_Mapper_form.cgi) with cut-off score equal to 3

>sp|O35047|HOP2_MOUSE Homologous-pairing protein 2 homolog OS=Mus musculus OX=10090
GN=Psmc3ip PE=1 SV=1

cNLS Mapper Result

Predicted NLSs in query sequence		
MSKSRAEAAAGAPGIILRYLQEQNRPYSAQDVFGNLQKEHGLGKAAVVKA	50	
LDQLAQEGKIKEKTYGKQKIYFADQNQFDTVSDADLHGLDASIVALTAKV	100	
QSLQQSCRHMEAEKELTSALTTPEMQKEIQELKKECAQYTERLKNIAA	150	
TNHVTPEEKEKVYRDRQKYCKEWRKRKRMTTELCDAILEGYPKSKKQFFE	200	
EVGIETDEHDHNVLLPDP	217	

Predicted monopartite NLS		
Pos.	Sequence	Score
172	EWKRKRKRMTTELC	6
172	EWKRKRKRMTT	8
174	RKRKRMTTE	3

Predicted bipartite NLS		
Pos.	Sequence	Score
39	EHGLGKAAVVKALDQLAQEGKIKEKTYGKQKIY	3.1
142	ERLKNIAATNHVTPEEKEKVYRDRQKYCKE	3.3
143	RLKNIAATNHVTPEEKEKVYRDRQKYCKEW	3.4
164	RDRQKYCKEWRKRKRMTTELCDAILEGYPKSKK	4.9
166	RQKYCKEWRKRKRMTTELCDAILEGYPKSKKQFFEE	3.2
171	KEWRKRKRMTTELCDAILEGYPKSKK	7.6
171	KEWRKRKRMTTELCDAILEGYPKSKKQF	5.2
171	KEWRKRKRMTTELCDAILEGYPKSKKQFFE	8.1
171	KEWRKRKRMTTELCDAILEGYPKSKKQFFEE	6.9
171	KEWRKRKRMTTELCDAILEGYPKSKKQFFEE	4.8
172	EWKRKRKRMTTELCDAILEGYPKSKK	6.4
172	EWKRKRKRMTTELCDAILEGYPKSKKQF	3.7
172	EWKRKRKRMTTELCDAILEGYPKSKKQFFE	8
172	EWKRKRKRMTTELCDAILEGYPKSKKQFFEE	6.1

>sp|P15927|RFA2_HUMAN Replication protein A 32 kDa subunit OS=Homo sapiens OX=9606
GN=RPA2 PE=1 SV=1

cNLS Mapper Result

Predicted NLSs in query sequence	
MWNSGFESYGSSSYGGAGGYTQSPGGFGSPAPSQAEEKSRARAQHIVPCT	50
ISQLLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIIVYKIDDMTAA	100
PMDVRQWVDTTSSSENTVVPPEYVVKVAGHLRSFQNKSLVAFKIMPLE	150
DMNEFTTHILEVINAHMVLKANSQPSAGRAPISNPGMSEAGNFGGNSFM	200
PANGLTVAQNQVLNLIKACPRPEGLNFQDLKNQLKHMSVSSI KQAVDFLS	250
NEGHIYSTVDDHFKSTDAE	270

Predicted monopartite NLS		
Pos.	Sequence	Score

Predicted bipartite NLS		
Pos.	Sequence	Score
243	KQAVDFLSNEGHIYSTVDDHFKSTDAE	3.5

>sp|Q12018|CDC53_YEAST Cell division control protein 53 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC53 PE=1 SV=1

Predicted NLSs in query sequence	
MSETLPRSDDEATWNFIEPGINQILGNEKNQASTSKRVYKILSPTMYME	50
VYTAIYNYCVNKSRRSSGHFSTDSRTGQSTILVGSEIYEKLKNYLKNYILN	100
FKQSNSETFLQFYVVKRWKRFTIGAIFLNHAFDYMNRVWQKERSDGKRHI	150
FDVNTLCLMTWKEVMFDPKDVLINELLDQVTLGREGQIIQRSNISTAIK	200
SLVALGIDPQDLKKLNLVYIQVFEKPFLLKKTQEYVTQYNDYLEKHSVT	250
EYIFEAEHIIKREEKAMTIYDDHTKKPLSMALNKVLITDHIEKLENEFV	300
VLLDARDIEKITSLYALIRRDFTLIPRMASVFENYVKKTGENEISSLLAM	350
HKHNIMKNENANPKKLALMTAHSLSPKDYIKKLEVDHIFSKIFNESFPD	400
DIPLAKALDNACGAFININEFALPAGSPKSATSKTSEMLAKYSDILLKKA	450
TKPEVASDMSDEDIITIFKYLTDKDAFETHYRRLFAKRLIHGTSTSAEDE	500
ENIIQRLQAANSMEYTGKITKMFQDIRLSKILEDDFAVALKNEDYSKAK	550
YPDLPQFVLAENMWPFYSQVEFEKLPKELVPSHEKLESYSQKHNGRILK	600
WLWPLCRGELKADIGKPGRMFPNFTVTLFQMAILLLYNDADVLTLENIQE	650
GTSLTIQHIAAAMVPFIKFKLIQQVPPGLDALVKPETQFKLSRPYKALKT	700
NINFASGVKNDILQSLSGGGHDNHGKNLGNKRLTEDERIEKELNTERQIF	750
LEACIVRIMKAKRNLPHHTLVNECIAQSHQRFNAKVS	800
YLQRGDDGESYAYLA	815

Predicted monopartite NLS		
Pos.	Sequence	Score

Predicted bipartite NLS		
Pos.	Sequence	Score
36	SKRVYKILSPTMYMEVYTAIYNYCVNK	3.2
37	KRVYKILSPTMYMEVYTAIYNYCVNKSRRSSG	3.2
88	EKLKNYLKNYILNFKQSNSETFLQFYVVKRWK	3.2
91	KNYLKNYILNFKQSNSETFLQFYVVKRWKRFTI	4
115	KRWKRFTIGAIFLNHAFDYMNRVWQKERSD	3.3
426	GSPKSATSKTSEMLAKYSDILLKKATKPE	3.7
426	GSPKSATSKTSEMLAKYSDILLKKATKPEV	3
482	RRLFAKRLIHGTSTSAEDEENIIQRLQAAN	3
482	RRLFAKRLIHGTSTSAEDEENIIQRLQAANSME	3.2
665	PFIKFKLIQQVPPGLDALVKPETQFKLSRPY	6.4
666	FIKFKLIQQVPPGLDALVKPETQFKLSRPY	3.3
709	KNDILQSLSGGGHDNHGKNLGNKRLTED	3.8
757	RIMKAKRNLPHHTLVNECIAQSHQRFNAKVS	3.6
757	RIMKAKRNLPHHTLVNECIAQSHQRFNAKVS	3
757	RIMKAKRNLPHHTLVNECIAQSHQRFNAKVSM	5
757	RIMKAKRNLPHHTLVNECIAQSHQRFNAKVMVK	3

>sp|Q13616|CUL1_HUMAN Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=2

Predicted NLSs in query sequence	
MSSTRSQNPGLKQIGLDQIWDDLRAQIQVYTRQSMASRYMELYTHVY	50
NYCTSVHQSNQARGAGVPPSKSKKGQTPGGAQFVGLELYKRLKEFLKNYL	100
TNLLKDGEDLMDESVLKFYTTQWEDYRFSSKVLNGICAYLNRHWRRECD	150
EGRKGIYEIYSLALVTWRDCLFRPLNKQVTNAVLKLIKERNGETINTRL	200
ISGVVQSYVELGLNEDDAFAKGPTLTVYKESFESQFLADTERFYTRETE	250
FLQQNPVTEYMKAEARLLEEQRVQVYLHESTQDELARKCEQVLIKHL	300
EIFHTEFQNLLDADKNEDLGRMYNLVSRIQDGLGELKKLLETHHNQGLA	350
AIEKCGEALNDPKMYVQTVLDVHKYNALVMSAFNNDAGFVAALDKACG	400
RFINNNAVTKMAQSSSKSPELLARYCDSLLKKSSKNPEEALEDTLNQVM	450
VVFYIEDKDVFKFYAKMLAKRLVHQNSASDDAEASMISKLKQACGFEY	500
TSKLQRMFQDIGVSKDLNEQFKKHLTNSEPLDLDFSIQVLSGSGWPFQQS	550
CTFALPSELEERSYQRTAFYASRHSGRKLTWLYQLSKGELVTNCFKNRYT	600
LQASTFQMAILLYNTEDAYTVQQLTDSTQIKMDILAQVLQILLKSKLLV	650
LEDENANVDEVELKPDTLIKLYLGYNKKLRVNINVPMKTEQKQEQTTH	700
KNIEEDRKLIIQAAIVRIMKMRKVLKHQQLLGEVLTQLSSRFKPRVPVIK	750
KCIDILIEKEYLERVDGEKDTYSYLA	776

Predicted monopartite NLS		
Pos.	Sequence	Score
673	LGYNKKLRVN	3

Predicted bipartite NLS		
Pos.	Sequence	Score
63	RGAGVPPSKSKKGQTPGGAQFVGLELYKRLKEFL	4.2
90	KRLKEFLKNYLTNLLKDGEDLMDESVLKFYT	3.3
91	RLKEFLKNYLTNLLKDGEDLMDESVLKFYT	4.9
91	RLKEFLKNYLTNLLKDGEDLMDESVLKFYTQQWE	3
146	RRECDGRKGIYEIYSLALVTWRDCLFRPLNKQVT	3
408	VTKMAQSSSKSPELLARYCDSLLKKSS	3.3
408	VTKMAQSSSKSPELLARYCDSLLKKSSKNP	6.7
424	RYCDSLLKKSSKNPEEALEDTLNQVMVVFYIEDK	4.5
464	KFYAKMLAKRLVHQNSASDDAEASMISKLK	3.1
468	KMLAKRLVHQNSASDDAEASMISKLKQA	3.5
468	KMLAKRLVHQNSASDDAEASMISKLKQACG	5.1
468	KMLAKRLVHQNSASDDAEASMISKLKQACGFE	3.7
489	ISKLKQACGFEYTSKLQRMFQDIGVSKDLNE	3.3
573	RHSGRKLTWLYQLSKGELVTNCFKNRYTLQAST	3
643	LLKSKLLVLEDENANVDEVELKPDTLIKLY	4.5
646	SKLLVLEDENANVDEVELKPDTLIKLYL	3.3
676	KNKKLRVNINVPMKTEQKQEQTTHKNIEED	4.1
697	ETTHKNIEEDRKLIIQAAIVRIMKMRKVLKH	6.3
717	RIMKMRKVLKHQQLLGEVLTQLSSRFKPRVP	4.4
717	RIMKMRKVLKHQQLLGEVLTQLSSRFKPRVPVIK	3.2
722	RKVLKHQQLLGEVLTQLSSRFKPRVPVIKKCI	4.6

>sp|Q9UJX6|ANC2_HUMAN Anaphase-promoting complex subunit 2 OS=Homo sapiens OX=9606
GN=ANAPC2 PE=1 SV=1

Predicted NLSs in query sequence	
MAAAVVVAEGSDSRPGQELLVAWNTVSTGLVPPAALGLVSSRTSGAVPP	50
KEELRAAVEVLRGHGLHSLVEEFVEVLQNDLQANISPEFWNAISQCEN	100
SADEPQCLLLLDAGLLESRLDPYLRSELELEKWTRLGLLMGTGAQGLR	150
EEVHTMLRGVLFFSTPRTFQEMIQRLYGCFLRVYMQSKRKGEAGTDPELE	200
GELDSRYARRRYRLLQSPLCAGCSSDKQQCWCRQALEQFHQLSQVLHRL	250
SLLERVSAAEAVTTTLHQVTRERMEDRCRGEYERSFLREFHKWIERVVGWL	300
GKVFLLQDGPAPASPEAGNTLRRWRCHVQRFFYRIYASLRIEELFSIVRD	350
FPDSRPAIEDLKYCLERTDQRQQLLVSLKAALETLLHPGVNTCDIITLY	400
ISAIKALRVLDPSMVILEVACEPIRRYLRTREDTVRQIVAGLTGDSGTG	450
DLAVELSKTDPASLETGQDSEDDSGEPEDWVPDPVDADPGKSSSKRRSSD	500
IISLLVSIYGSKDLFINEYRSLADRLHQFSFPEREIRNVELLKLRFG	550
EAPMHFCEVMLKDMADSRINANIREEDEKRPAAEQPPFGVYAVILSSEF	600
WPPFKDEKLEVPEDIRAALAYCKKYEQLKAMRTLQWHTLGLVTMDVEL	650
ADRTLSVAVTPVQAVILLYFQDQASWTLLELSKAVKMPVALLRRRMSVWL	700
QQGVLREPPPGTFVIEEERPQDRDNMVLIDSDESDSGMASQADQKEEE	750
LLLFWTYIQAMLTNLESLSLDRIYNMLRMFVVTGPALAEIDLQELQGYLQ	800
KKVRDQQLVYSAGVYRLPKNCS	822

Predicted monopartite NLS		
Pos.	Sequence	Score

Predicted bipartite NLS		
Pos.	Sequence	Score
182	RVYMQSKRKGEAGTDPELEGEELDSRYARR	5.1
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRY	5.6
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRYR	6.7
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRYR	7.8
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRYR	6.7
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRYR	3
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRYRLL	3.2
182	RVYMQSKRKGEAGTDPELEGEELDSRYARRRYRLL	3.9
204	DSRYARRRYRLLQSPLCAGCSSDKQQCWCR	3.8
206	RYARRRYRLLQSPLCAGCSSDKQQCWCRQALE	4
206	RYARRRYRLLQSPLCAGCSSDKQQCWCRQALE	3.2
295	RVVGWLGKVFLLQDGPAPASPEAGNTLRRWRCHV	3.7
401	ISAIKALRVLDPSMVILEVACEPIRRYLRT	3.5
401	ISAIKALRVLDPSMVILEVACEPIRRYLRTRE	3.4
491	KSSSKRRSSDIISLLVSIYGSKDLFINEYR	3.4
540	RNVELLKLRFGEAPMHFCEVMLKDMADSRINA	4.2
604	FKDEKLEVPEDIRAALAYCKKYEQLKAMRT	3.2

>sp|Q12158|SCC1_YEAST Sister chromatid cohesion protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCD1 PE=1 SV=1

Predicted NLSs in query sequence	
MVTENPQRLTVLRLATNKGPLAQIWLASNMSNIPRGSVIQTHIAESAKEI	50
AKASGCDDDESGDNEYITLRTSGELLQGIVRVYSKQATFLLTDIKDTLTKI	100
SMLFKTSQKMTSTVNRLNTVTRVHQLMLEDAVTEREVLVTPGLEFLDDTT	150
IPVGLMAQENSMEKVKQGAAPWDTSLVGRRFSPDEDFEHNLSMNLDF	200
DIEEGPITSKSWEEGTRQSSRNFDTHENYIQDDDFPLDDAGTIGWDLGIT	250
EKNDQNDDDDNSVEQGRRLGESIMSEPTDFGFDLDIEKEAPAGNIDI	300
TDAMTESQPKQTGTRRNSKLLNTKSIQIDEETENSESIASNTYKEERSN	350
NLLTPQPTN FTTKRLWSEITESMSYLPDPILKNFLSYESLKKRKIH NGRE	400
GSIEEPELNVSLNLTDDVISNAGTNDNSFNELTDNMSDFVPIDAGLNEAP	450
FPEENIIDAKTRNEQTTIQTEKVRPTPGEVASKAIVQMAKILRKELSEEK	500
EVIFTDVLKSQANTEPENITKREASRGFFDILSLATEGCIGLSQTEAFGN	550
IKIDAKPALFERFINA	566

Predicted monopartite NLS		
Pos.	Sequence	Score
387	YESLKKRKIH	6.5

Predicted bipartite NLS		
Pos.	Sequence	Score
360	FTTKRLWSEITESMSYLPDPILKNFLSY	5.5
360	FTTKRLWSEITESMSYLPDPILKNFLSYE	3.8

>sp|Q12440|APC2_YEAST Anaphase-promoting complex subunit 2 OS=Saccharomyces cerevisiae
(strain ATCC 204508 / S288c) OX=559292 GN=APC2 PE=1 SV=1

Predicted NLSs in query sequence	
MSFQITPTRDLKQITDELQTLSSYIFHTNIVDDLNSLLTWMSPNDAKSNH	50
QLRPPSLRIKNIKVLFPNNATTSPYSMINTSQANNSIVNEGNTNKLQL	100
QLFSTLKEFYIFQVRYHFFLHFNNINYLKDIQRWENYYEPLRYVPIFDV	150
NVNDWALELNSLRHYLLNRNIKFKNNLRTRLDKLIMDDDFDLADNLIQWL	200
KSANGSLSSTELIVNALYSKINKFCEDNMSRVWNKRFMIMETFNKFQY	250
WSQFSKLVGCPEDDHELTTTFVNCFSNFLRIRTNEIFDICVLAYPDSKV	300
TLLELRKIMKDFKDYTNIVTTFLSDFKKYILNPSVTTVDALLRYVVTIKA	350
FLVLDPTGRCLHSITTFVKPYFQERKHLNVNLLYAMLDLPEEELKEKINF	400
NVDMKALLSLVDTLHDSINQDTNITKRDKNKSPFLWNLVKVGKRELNK	450
DLPIRHAMLYEHILNYYIAWVPEPNDMIPGNIKSSYIKTNLFEVLLDLFE	500
SREFFISEFRNLLTDRLFTLKFYTLDEKWTRCLKLIREKIVKFTETS	550
YITNGILGLLETTAPAADADQSNLNSIDVMLWDIKCSEELCRKMHEVAGL	600
DPIIFPKFISLLWKYNCDTQGSNDLAFHLPIDLERELQKYSDIYSQLKP	650
GRKLQLCKDKGKVEIQAFKDGRLVLDVLEQCSVINQFDSNPDEPICL	700
SLEQLSESLNIAPPRLTHLLDFWIQGVLLKENGTVSVIEHSEMDFDQAQ	750
KTAPMEIENSNYELHNDSEIERKYELTLQRSLPFIEGMLTNLGAMKLHKI	800
HSFLKITVPKDWGNRITLQQLLEGYLNTLADEGRKYIANGSYEIVKNGH	850
KNS	853

Predicted monopartite NLS

Pos.	Sequence	Score

Predicted bipartite NLS

Pos.	Sequence	Score
103	FSTLKEFYIFQVRYHFFLHFNNINYLKDIQRW	3.3
169	RNIKFKNNLRTRLDKLIMDDDFDLADNLIQWLK	3.7
174	KNNLRTRLDKLIMDDDFDLADNLIQWLKSAN	3.6
197	IQWLKSANGSLSSTELIVNALYSKINKFCED	3.2
220	KINKFCEDNMSRVWNKRFMIMETFNKFQY	3
231	RVWNKRFMIMETFNKFQYWSQFSKLVGCP	4.9
231	RVWNKRFMIMETFNKFQYWSQFSKLVGCP	3.4
304	ELRKIMKDFKDYTNIVTTFLSDFKKYILNP	3
325	DFKKYILNPSVTTVDALLRYVVTIKAFV	3.7
372	FQERKHLNVNLLYAMLDLPEEELKEKINFN	3
372	FQERKHLNVNLLYAMLDLPEEELKEKINFNV	4.1
428	RDKNKSPFLWNLVKVGKRELNKDLPIRHAMLY	3
441	KVGKRELNKDLPIRHAMLYEHILNYYIAWV	4
486	YIKTNLFEVLLDLFESREFFISEFRNLLTD	3.4
516	RLFTLKFYTLDEKWTRCLKLIREKIVKFTETS	3.1
582	WDIKCSEELCRKMHEVAGLDPIIFPKFISL	3.3
588	EELCRKMHEVAGLDPIIFPKFISLLWKYNCDT	3.2
649	KPGRKLQLCKDKGKVEIQAFKDGRLVLD	3.7
649	KPGRKLQLCKDKGKVEIQAFKDGRLVLDVS	3.1
747	DQAQKTAPMEIENSNYELHNDSEIERKYELT	3.8

>sp|Q921X6|RPC6_MOUSE DNA-directed RNA polymerase III subunit RPC6 OS=Mus musculus
OX=10090 GN=Polr3f PE=1 SV=1

Predicted NLSs in query sequence	
MAEVKVKVQPPDADPVEIENRIELCHQFPHGITDQVIQNEMPHIEAQQR	50
AVAINRLLSMGQLDLLRSNTGLLYRIKDSQAGKMKGSDNQEKL VYQIIE	100
DAGNKGIWSRDIRYKSNLPLTEINKILKNLESKKLIKAVKSVAAASKKKVY	150
MLYNLQPDRSVTGGAWYSDQDFESEFVEVLNQQCFKFLQSKAETARESKQ	200
NPVIQRNSSFASSHEVWKYICELGISKVELSMEDIETILNTLIYDGK VEM	250
TIIAAKEGTVGSVDGHMKLYRAVNPILPPTGVVRAPCGLCPVFEDCHEGG	300
EISPSNCIYMTWLEF	316

Predicted monopartite NLS		
Pos.	Sequence	Score

Predicted bipartite NLS		
Pos.	Sequence	Score
110	RDIRYKSNLPLTEINKILKNLESKKLIKA	4.1
110	RDIRYKSNLPLTEINKILKNLESKKLIKA	5.3
110	RDIRYKSNLPLTEINKILKNLESKKLIKAVK	6.9
122	EINKILKNLESKKLIKAVKSVAAASKKKVYM	3.2